

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Philip E.Branton et al.
5 (ii) TITLE OF THE INVENTION: Adenovirus E4 Protein For
Inducing Cell Death

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 3 July 1997
(C) CLASSIFICATION:

25 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/021,273
(B) FILING DATE: 5 July 1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/028,740
(B) FILING DATE: 22 October 1996

30 (ix) ATTORNEY/AGENT INFORMATION:

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35 (x) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGACTACGT CGGGCGTTCC ATTTGGCATG ACACATCGAC CAACACGATC TCGGTTGTCT	60
CGGCGCACTC CGTACAGTAG GGATCGTCTA CCTCCTTTG AGACAGAAAC CCGCGCTACC	120
ATACTGGAGG ATCATCCGCT GCTGCCGAA TGTAACACTT TGACAATGCA CAACGTGAGT	180
10 TACGTGCGAG GTCTTCCCTG CAGTGTGGGA TTTACGCTGA TTCAGGAATG GGTTGTTCCC	240
TGGGATATGG TTCTAACCGG GGAGGAGCTT GTAATCCTGA GGAAGTGTAT GCACGTGTGC	300
CTGTGTTGTG CCAACATTGA TATCATGACG AGCATGATGA TCCATGGTTA CGAGTCCTGG	360
GCTCTCCACT GTCATTGTTG CAGTCCCAGT TCCCTGCGAGT GTATAGCCGG CGGGCAGGTT	420
TTGGCCAGCT GGTTTAGGAT GGTGGTGGAT GGCGCCATGT TTAATCAGAG GTTTATATGG	480
15 TACCGGGAGG TGGTGAATTAA AACATGCCA AAAGAGGTAA TGTTTATGTC CAGCGTGT	540
ATGAGGGGTC GCCACTTAAT CTACCTGCGC TTGTGGTATG ATGGCCACGT GGGTTCTGTG	600
GTCCCCGCCA TGAGCTTGG ATACAGCGCC TTGCACTGTG GGATTTGAA CAATATTGTG	660
GTGCTGTGCT GCAGTTACTG TGCTGATTAA AGTGAGATCA GGGTGCCTG CTGTGCCCGG	720
AGGACAAGGC GCCTTATGCT GCGGGCGGTG CGAACATCG CTGAGGAGAC CACTGCCATG	780
20 TTGTATTCT GCAGGACGGA GCGGCCGCGG CAGCAGTTA TTCGCGCGCT GCTGCAGCAC	840
CACCGCCCTA TCCTGATGCA CGATTATGAC TCTACCCCCA TGTAG	885

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 Met Thr Thr Ser Gly Val Pro Phe Gly Met Thr Leu Arg Pro Thr Arg	
1 5 10 15	
Ser Arg Leu Ser Arg Arg Thr Pro Tyr Ser Arg Asp Arg Leu Pro Pro	
20 25 30	
Phe Glu Thr Glu Thr Arg Ala Thr Ile Leu Glu Asp His Pro Leu Leu	
35 40 45	
Pro Glu Cys Asn Thr Leu Thr Met His Asn Val Ser Tyr Val Arg Gly	
50 55 60	
Leu Pro Cys Ser Val Gly Phe Thr Leu Ile Gln Glu Trp Val Val Pro	
65 70 75 80	
Trp Asp Met Val Leu Thr Arg Glu Glu Leu Val Ile Leu Arg Lys Cys	
85 90 95	
Met His Val Cys Leu Cys Cys Ala Asn Ile Asp Ile Met Thr Ser Met	
100 105 110	
Met Ile His Gly Tyr Glu Ser Trp Ala Leu His Cys His Cys Ser Ser	
115 120 125	
45 Pro Gly Ser Leu Gln Cys Ile Ala Gly Gly Gln Val Leu Ala Ser Trp	
130 135 140	

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTTCTTC	CAGCTCTTCC	CGCTCCTCCC	GTGTGTGACT	CCGAGAACGA	ATGTGTAGGT	60
TGGCTGGGTG	TGGCTTATTG	TGCGGTGGTG	GATGTTATCA	GGGCAGCGGC	GCATGAAGGA	120
GT TTACATAG	AACCCGAAGC	CAGGGGGCGC	CTGGATGCTT	TGAGAGAGTG	GATATACTAC	180
AACTACTACA	CAGAGCGATC	TAAGCGGCCA	GACCGGAGAC	GCAGATCTGT	TTGTCA CGCC	240
CGCACCTGGT	TTTGCTTCAG	GAATATGAC	TACGTCCGGC	GTTC CATTG	GCATGACACT	300
ACGACCAAACA	CGATCTCGGT	TGTCTCGGCC	CACTCCGTAC	AGTAG		345

35 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Leu	Pro	Ala	Leu	Pro	Ala	Pro	Pro	Val	Cys	Asp	Ser	Gln	Asn
1				5					10					15	

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Glu Cys Val Gly Trp Leu Gly Val Ala Tyr Ser Ala Val Val Asp Val
20 25 30
Ile Arg Ala Ala Ala His Glu Gly Val Tyr Ile Glu Pro Glu Ala Arg
35 40 45
5 Gly Arg Leu Asp Ala Leu Arg Glu Trp Ile Tyr Tyr Asn Tyr Tyr Thr
50 55 60
Glu Arg Ser Lys Arg Arg Asp Arg Arg Arg Ser Val Cys His Ala
65 70 75 80
10 Arg Thr Trp Phe Cys Phe Arg Lys Tyr Asp Tyr Val Arg Arg Ser Ile
85 90 95
Trp His Asp Thr Thr Thr Asn Thr Ile Ser Val Val Ser Ala His Ser
100 105 110
Val Gln

What is claimed is:

1. A recombinant DNA molecule comprising a nucleic acid sequence which encodes a polypeptide having the amino acid sequence set forth above.